```
aattgtggct gtggaactgt caactggagg tcctgcacat gcaattcagg gaaaaccgtg 60
aaaaagtatc atgaggtatt acagtttgag cctggccaca tcaagaggag ggtagagct 120
aagaccatgg ctctagttga catccagttg gatcaccatg aacgatgtga ttgtatctgc 180
agctcaagac cacctcgata agagaatgtg cacatcctta cattaagcct gaaagaacca 240
ttagtttaag gagggtgaga taagagaccc ttttcctacc agcaaccaga cttactacta 300
gcctgcaatg caatgaacac aagtggttgc tgagtctcag ccttgctttg ttaatgccat 360
```

Fig. 1


```
Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
 1               5                   10                  15

Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
            20                  25                  30

His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
        35                  40                  45

Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
    50                  55                  60

Pro Arg
65
```

Fig. 2

```
ggaagatttc caacccgcag cagcttcaga gaccaactgg aatctgtcac aagctctgtt 60
tcagggtatc cctataactc tccatcagta acggatccca ctctgattgc ggatgctctg 120
gacaaaaaaa ttgcagaatt tgatacagtg gaagatctgc tcaagtactt caatccagag 180
tcatggcaag aagatcttga gaatatgtat ctggacaccc ctcggtatcg aggcaggtca 240
taccatgacc ggaagtcaaa agttgacctg gataggctca atgatgatgc caagcgttac 300
agttgcactc ccaggaatta ctcggtcaat ataagagaag agctgaagtt ggccaatgtg 360
gtcttctttc cacgttgcct cctcgtgcag cgctgtggag gaaattgtgg ctgtggaact 420
gtcaaactgg agtcctgcac atgcaattca gggaaaaccg tgaaaaagta tcatgaggta 480
ttacagtttg agcctggcca catcaagagg aggggtagag ctaagaccat ggctctagtt 540
gacatccagt tggatcacca tgaacgatgc gattgtatct gcagctcaag accacctcga 600
taagagaatg tgcacatcct tacattaagc ctgaaagaac ctttagttta aggagggtga 660
gataagagac ccttttccta ccagcaaccc                                  690
```

Fig. 3

```
Gly Arg Phe Pro Thr Arg Ser Ser Phe Arg Asp Gln Leu Glu Ser Val
  1               5                  10                  15

Thr Ser Ser Val Ser Gly Tyr Pro Tyr Asn Ser Pro Ser Val Thr Asp
            20                  25                  30

Pro Thr Leu Ile Ala Asp Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp
        35                  40                  45

Thr Val Glu Asp Leu Leu Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu
    50                  55                  60

Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser
65                  70                  75                  80

Tyr His Asp Arg Lys Ser Lys Val Asp Leu Asp Arg Leu Asn Asp Asp
                85                  90                  95

Ala Lys Arg Tyr Ser Cys Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg
            100                 105                 110

Glu Glu Leu Lys Leu Ala Asn Val Val Phe Phe Pro Arg Cys Leu Leu
        115                 120                 125

Val Gln Arg Cys Gly Gly Asn Cys Gly Cys Gly Thr Val Lys Leu Glu
    130                 135                 140

Ser Cys Thr Cys Asn Ser Gly Lys Thr Val Lys Lys Tyr His Glu Val
145                 150                 155                 160

Leu Gln Phe Glu Pro Gly His Ile Lys Arg Arg Gly Arg Ala Lys Thr
                165                 170                 175

Met Ala Leu Val Asp Ile Gln Leu Asp His His Glu Arg Cys Asp Cys
            180                 185                 190

Ile Cys Ser Ser Arg Pro Pro Arg
        195                 200
```

Fig. 4

```
ttgtaccgaa gagatgagac catccaggtg aaaggaaacg gctacgtgca gagtcctaga 60
ttcccgaaca gctaccccag gaacctgctc ctgacatggc ggcttcactc tcaggagaat 120
acacggatac agctagtgtt tgacaatcag tttggattag aggaagcaga aaatgatatc 180
tgtaggtatg attttgtgga agttgaagat atatccgaaa ccagtaccat tattagagga 240
cgatggtgtg gacacaagga agttcctcca aggataaaat caagaacgaa ccaaattaaa 300
atcacattca agtccgatga ctactttgtg gctaaacctg gattcaagat ttattattct 360
ttgctggaag atttccaacc cgcagcagct tcagagacca actgggaatc tgtcacaagc 420
tctatttcag gggtatccta taactctcca tcagtaacgg atcccactct gattgcggat 480
gctctggaca aaaaaattgc agaatttgat acagtggaag atctgctcaa gtacttcaat 540
ccagagtcat ggcaagaaga tcttgagaat atgtatctgg acacccctcg gtatcgaggc 600
aggtcatacc atgaccggaa gtcaaaagtt gacctggata ggctcaatga tgatgccaag 660
cgttacagtt gcactcccag gaattactcg gtcaatataa gagaagagct gaagttggcc 720
aatgtggtct tctttccacg ttgcctcctc gtgcagcgct gtggaggaaa ttgtggctgt 780
ggaactgtca actggaggtc ctgcacatgc aattcaggga aaaccgtgaa aaagtatcat 840
gaggtattac agtttgagcc tggccacatc aagaggaggg gtagagctaa gaccatggct 900
ctagttgaca tccagttgga tcaccatgaa cgatgcgatt gtatctgcag ctcaagacca 960
cctcgataag agaatgtgca catccttaca ttaagcctga aagaaccttt agtttaagga 1020
gggtgagata agagaccctt ttcctaccag caaccaaact tactactagc ctgcaatgca 1080
atgaacacaa gtggttgctg agtctcagcc ttgctttgtt aatgccatgg caagtagaaa 1140
ggtatatcat caacttctat acctaagaat ataggattgc atttaataat agtgtttgag 1200
gttatatatg cacaaacaca cacagaaata tattcatgtc tatgtgtata tagatcaaat 1260
gtttttttg gtatatataa ccaggtacac cagagcttac atatgtttga gttagactct 1320
taaaatcctt tgccaaaata agggatggtc aaatatatga aacatgtctt tagaaaattt 1380
aggagataaa tttatttta aatttgaaa cacaaaacaa ttttgaatct tgctctctta 1440
aagaaagcat cttgtatatt aaaaatcaaa agatgaggct ttcttacata tacatcttag 1500
ttgattatta aaaaaggaaa aaggtttcca gagaaaaggc caatacctaa gcatttttc 1560
catgagaagc actgcatact tacctatgtg gactgtaata acctgtctcc aaaaccatgc 1620
cataataata taagtgcttt agaaattaaa tcattgtgtt ttttatgcat tttgctgagg 1680
catccttatt catttaacac ctatctcaaa aacttactta gaaggttttt tattatagtc 1740
ctacaaaaga caatgtataa gctgtaacag aattttgaat tgtttttctt tgcaaaaccc 1800
ctccacaaaa gcaaatcctt tcaagaatgg catgggcatt ctgtatgaac ctttccagat 1860
ggtgttcagt gaaagatgtg ggtagttgag aacttaaaaa gtgaacattg aaacatcgac 1920
gtaactggaa accg                                                   1934
```

Fig. 5

```
Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
 1               5                  10                  15

Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
            20                  25                  30

Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
        35                  40                  45

Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
    50                  55                  60

Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
65                  70                  75                  80

Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
                85                  90                  95
```

Fig. 6

Fig. 6 cont.

```
Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
            100                 105                 110

Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
        115                 120                 125

Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
    130                 135                 140

Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
145                 150                 155                 160

Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
                165                 170                 175

Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
            180                 185                 190

Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
        195                 200                 205

Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
    210                 215                 220

Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
225                 230                 235                 240

Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
                245                 250                 255

Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
            260                 265                 270

Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
        275                 280                 285

His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
    290                 295                 300

Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
305                 310                 315                 320

Pro Arg
```

```
cgctcggaaa gttcagcatg caggaagttt ggggagagct cggcgattag cacagcgacc  60
cgggccagcg cagggcgagc gcaggcggcg agagcgcagg gcggcgcggc gtcggtcccg 120
ggagcagaac ccggcttttt cttggagcga cgctgtctct agtcgctgat cccaa       175

atg cac cgg ctc atc ttt gtc tac act cta atc tgc gca aac ttt tgc   223
Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys
  1               5                  10                  15

agc tgt cgg gac act tct gca acc ccg cag agc gca tcc atc aaa gct   271
Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala
             20                  25                  30

ttg cgc aac gcc aac ctc agg cga gat gag agc aat cac ctc aca gac   319
Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
         35                  40                  45

ttg tac cga aga gat gag acc atc cag gtg aaa gga aac ggc tac gtg   367
Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
     50                  55                  60

cag agt cct aga ttc ccg aac agc tac ccc agg aac ctg ctc ctg aca   415
Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
 65                  70                  75                  80

tgg cgg ctt cac tct cag gag aat aca cgg ata cag cta gtg ttt gac   463
Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
                 85                  90                  95

aat cag ttt gga tta gag gaa gca gaa aat gat atc tgt agg tat gat   511
Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
            100                 105                 110

ttt gtg gaa gtt gaa gat ata tcc gaa acc agt acc att att aga gga   559
Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
        115                 120                 125

cga tgg tgt gga cac aag gaa gtt cct cca agg ata aaa tca aga acg   607
Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
    130                 135                 140

aac caa att aaa atc aca ttc aag tcc gat gac tac ttt gtg gct aaa   655
Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
145                 150                 155                 160
```

Fig. 7

Fig. 7 cont.

```
cct gga ttc aag att tat tat tct ttg ctg gaa gat ttc caa ccc gca    703
Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
                165                 170                 175

gca gct tca gag acc aac tgg gaa tct gtc aca agc tct att tca ggg    751
Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
            180                 185                 190

gta tcc tat aac tct cca tca gta acg gat ccc act ctg att gcg gat    799
Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
        195                 200                 205

gct ctg gac aaa aaa att gca gaa ttt gat aca gtg gaa gat ctg ctc    847
Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
    210                 215                 220

aag tac ttc aat cca gag tca tgg caa gaa gat ctt gag aat atg tat    895
Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
225                 230                 235                 240

ctg gac acc cct cgg tat cga ggc agg tca tac cat gac cgg aag tca    943
Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
                245                 250                 255

aaa gtt gac ctg gat agg ctc aat gat gat gcc aag cgt tac agt tgc    991
Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
            260                 265                 270

act ccc agg aat tac tcg gtc aat ata aga gaa gag ctg aag ttg gcc    1039
Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
        275                 280                 285

aat gtg gtc ttc ttt cca cgt tgc ctc ctc gtg cag cgc tgt gga gga    1087
Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
    290                 295                 300

aat tgt ggc tgt gga act gtc aac tgg agg tcc tgc aca tgc aat tca    1135
Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
305                 310                 315                 320

ggg aaa acc gtg aaa aag tat cat gag gta tta cag ttt gag cct ggc    1183
Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
                325                 330                 335
```

Fig. 7 cont.

```
cac atc aag agg agg ggt aga gct aag acc atg gct cta gtt gac atc   1231
His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
            340                 345                 350

cag ttg gat cac cat gaa cga tgc gat tgt atc tgc agc tca aga cca   1279
Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
        355                 360                 365

cct cga taagagaatg tgcacatcct tacattaagc ctgaaagaac ctttagttta    1335
Pro Arg
    370

aggagggtga gataagagac ccttttccta ccagcaacca aacttactac tagcctgcaa 1395
tgcaatgaac acaagtggtt gctgagtctc agccttgctt tgttaatgcc atggcaagta 1455
gaaaggtata tcatcaactt ctatacctaa gaatatagga ttgcatttaa taatagtgtt 1515
tgaggttata tatgcacaaa cacacacaga aatatattca tgtctatgtg tatatagatc 1575
aaatgttttt tttggtatat ataaccaggt acaccagagc ttacatatgt ttgagttaga 1635
ctcttaaaat cctttgccaa aataagggat ggtcaaatat atgaaacatg tctttagaaa 1695
atttaggaga taaatttatt tttaaatttt gaaacacaaa acaattttga atcttgctct 1755
cttaaagaaa gcatcttgta tattaaaaat caaaagatga ggctttctta catatacatc 1815
ttagttgatt attaaaaaag gaaaaggtt tccagagaaa aggccaatac ctaagcattt 1875
tttccatgag aagcactgca tacttaccta tgtggactgt aataacctgt ctccaaaacc 1935
atgccataat aatataagtg ctttagaaat taaatcattg tgttttttat gcattttgct 1995
gaggcatcct tattcattta acacctatct caaaaactta cttagaaggt tttttattat 2055
agtcctacaa aagacaatgt ataagctgta acagaatttt gaattgtttt tctttgcaaa 2115
acccctccac aaaagcaaat cctttcaaga atggcatggg cattctgtat gaacctttcc 2175
agatggtgtt cagtgaaaga tgtgggtagt tgagaactta aaaagtgaac attgaaacat 2235
cgacgtaact ggaaaccg                                               2253
```

Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe
1 5 10 15

Cys Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys
20 25 30

Ala Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr
35 40 45

Asp Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr
50 55 60

Val Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu
65 70 75

Thr Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe
80 85 90 95

Asp Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr
100 105 110

Asp Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg
115 120 125

Gly Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg
130 135 140

Thr Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala
145 150 155

Lys Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro
160 165 170 175

Ala Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser
180 185 190

Gly Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala
195 200 205

Asp Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu
210 215 220

Leu Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met
225 230 235

Fig. 8

Fig. 8 cont.

```
Tyr Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys
240                 245                 250                 255

Ser Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser
                260                 265                 270

Cys Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu
            275                 280                 285

Ala Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly
        290                 295                 300

Gly Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn
    305                 310                 315

Ser Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro
320                 325                 330                 335

Gly His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp
                340                 345                 350

Ile Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg
            355                 360                 365

Pro Pro Arg
        370
```

```
PDGF-D  MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRR  40
PDGF-C  MSLFGLLLVTSALAGQRRGTQA-------ESNLSSKFQFSS  34

PDGF-D  D-ESNHLTDLYRRDETIQVKGNGYVQSPRFPNSYPRNLLL  79
PDGF-C  NKEQNGVQDPQHERIIT-VSTNGSIHSPRFPHTYPRNTVL  73

PDGF-D  TWRL-HSQENTRIQLVFDNQFGLEEAENDICRYDFVEVED  118
PDGF-C  VWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE  113

PDGF-D  ISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFV  158
PDGF-C  PSD--GTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFP  151

PDGF-D  AKPGFKIYYSLLEDFQPAAASETNWESVTSSISGVSYNSP  198
PDGF-C  SEPGFCIHYNIVMPQFTEAV------------------SP  173

PDGF-D  SVTDP-TLIADALDKKIAEFDTVEDLLKYFNPESWQEDLE  237
PDGF-C  SVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERWQLDLE  213

PDGF-D  NMYLDTPRYRGRSYHD-RKSKVDLDRLN-DDAKRYSCTPR  275
PDGF-C  DLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPR  253

PDGF-D  NYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRS  315
PDGF-C  NFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNE  293

PDGF-D  CTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLD  355
PDGF-C  CQCVPSKVTKKYHEVLQLRP-KTGVRG--LHKSLTDVALE  330

PDGF-D  HHERCDCICSSRPPR                          370
PDGF-C  HHEECDCVCRGSTGG                          345
```

Fig. 9

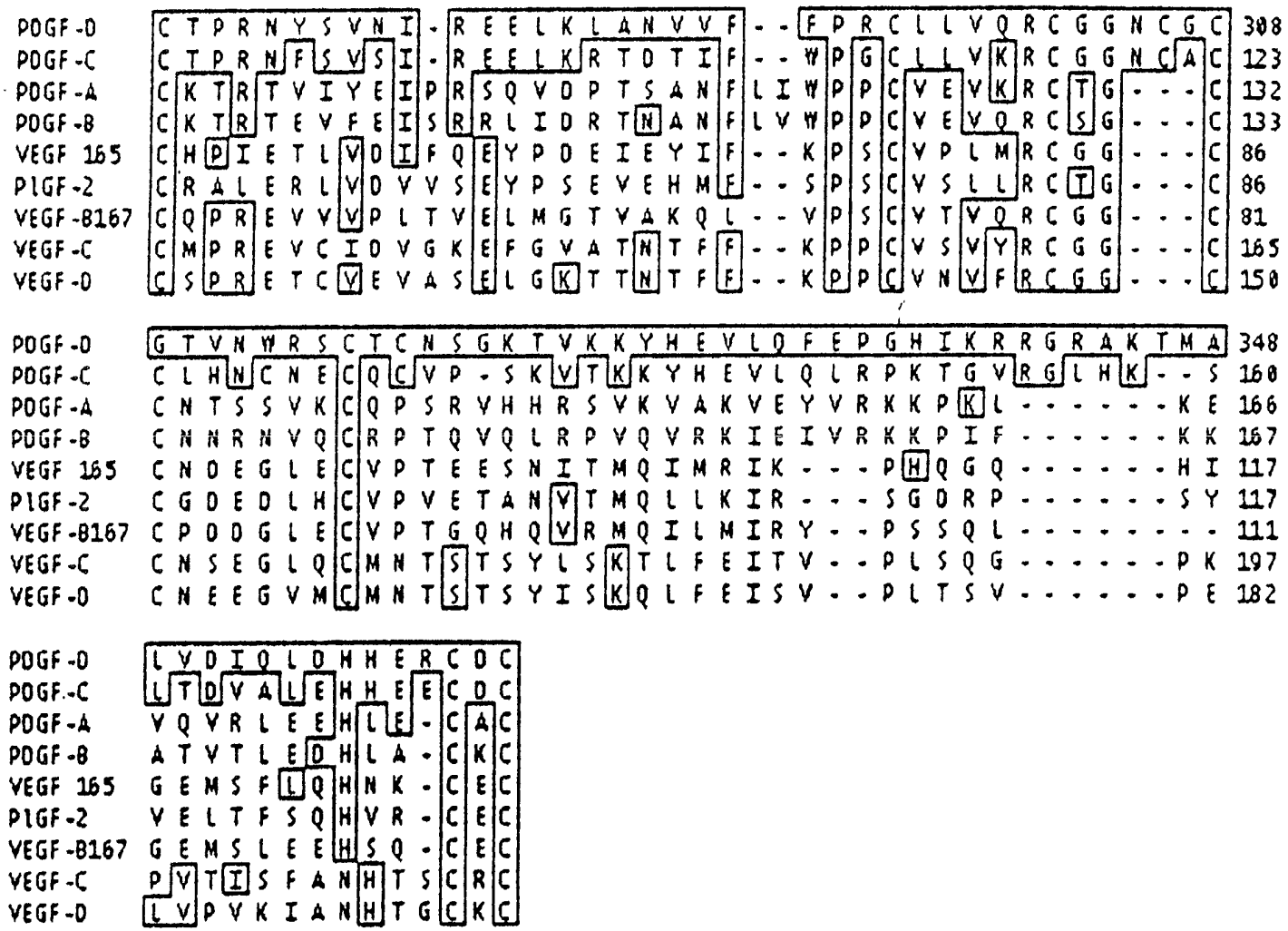

PDGF-D CTPRNYSVNI-REELKLANVVF--FPRCLLVQRCGGNCGC 308
PDGF-C CTPRNFSVSI-REELKRTDTIF--WPGCLLVKRCGGNCAC 123
PDGF-A CKTRTVIYEIPRSQVDPTSANFLIWPPCVEVKRCTG---C 132
PDGF-B CKTRTEVFEISRRLIDRTNANFLVWPPCVEVQRCSG---C 133
VEGF 165 CHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGG---C 86
PlGF-2 CRALERLVDVVSEYPSEVEHMFSPSCVSLLRCTG---C 86
VEGF-B167 CQPREVVVPLTVELMGTVAKQL--VPSCVTVQRCGG---C 81
VEGF-C CMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGG---C 165
VEGF-D CSPRETCVEVASELGKTTNTFFKPPCVNVFRCGG---C 150
PDGF-D GTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 348
PDGF-C CLHNCNECQCVP-SKVTKKYHEVLQLRPKTGVRGLHK--S 160
PDGF-A CNTSSVKCQPSRVHHRSVKVAKVEYVRKKPKL-------KE 166
PDGF-B CNNRNVQCRPTQVQLRPVQVRKIEIVRKKPIF-------KK 167
VEGF 165 CNDEGLECVPTEESNITMQIMRIK---PHQGQ-------HI 117
PlGF-2 CGDEDLHCVPVETANVTMQLLKIR---SGDRP-------SY 117
VEGF-B167 CPDDGLECVPTGQHQVRMQILMIRY--PSSQL---------- 111
VEGF-C CNSEGLQCMNTSTSYLSKTLFEITV--PLSQG-------PK 197
VEGF-D CNEEGVMCMNTSTSYISKQLFEISV--PLTSV-------PE 182
PDGF-D LVDIQLDHHERCDC
PDGF-C LTDVALEHHEECDC
PDGF-A VQVRLEEHLE-CAC
PDGF-B ATVTLEDHLA-CKC
VEGF 165 GEMSFLQHNK-CEC
PlGF-2 VELTFSQHVR-CEC
VEGF-B167 GEMSLEEHSQ-CEC
VEGF-C PVTISFANHTS CRC
VEGF-D LVPVKIANHTG CKC

Fig. 10

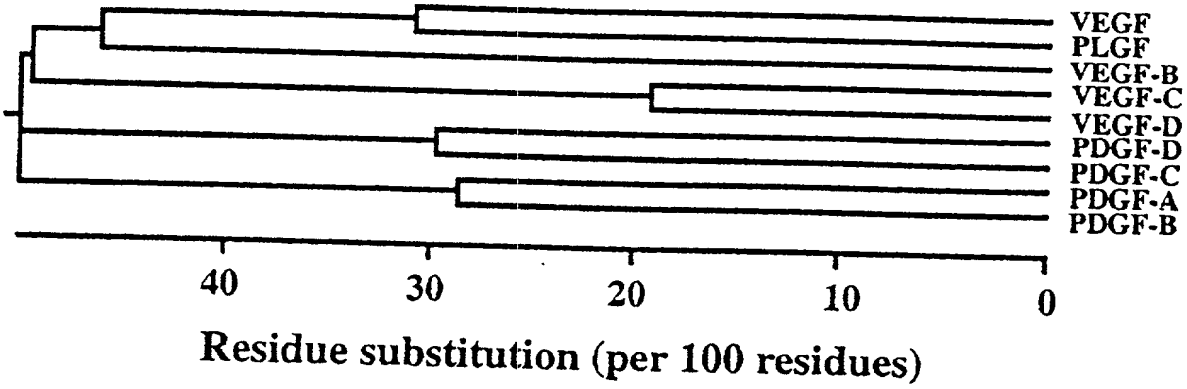

VEGF
PLGF
VEGF-B
VEGF-C
VEGF-D
PDGF-D
PDGF-C
PDGF-A
PDGF-B
40
30
20
10
0
Residue substitution (per 100 residues)

Fig. 11

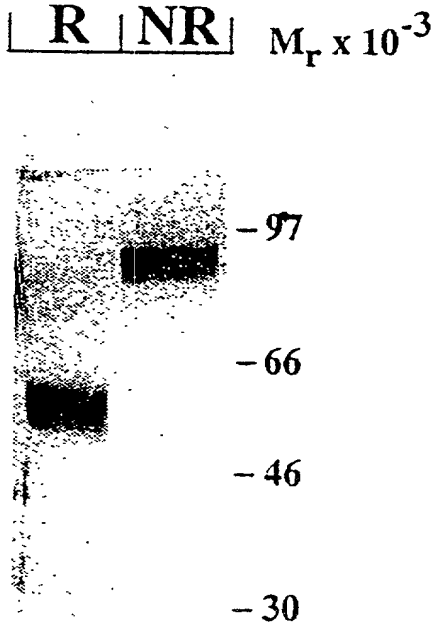

R
NR
$M_r \times 10^{-3}$
97
66
46
30

Fig. 13

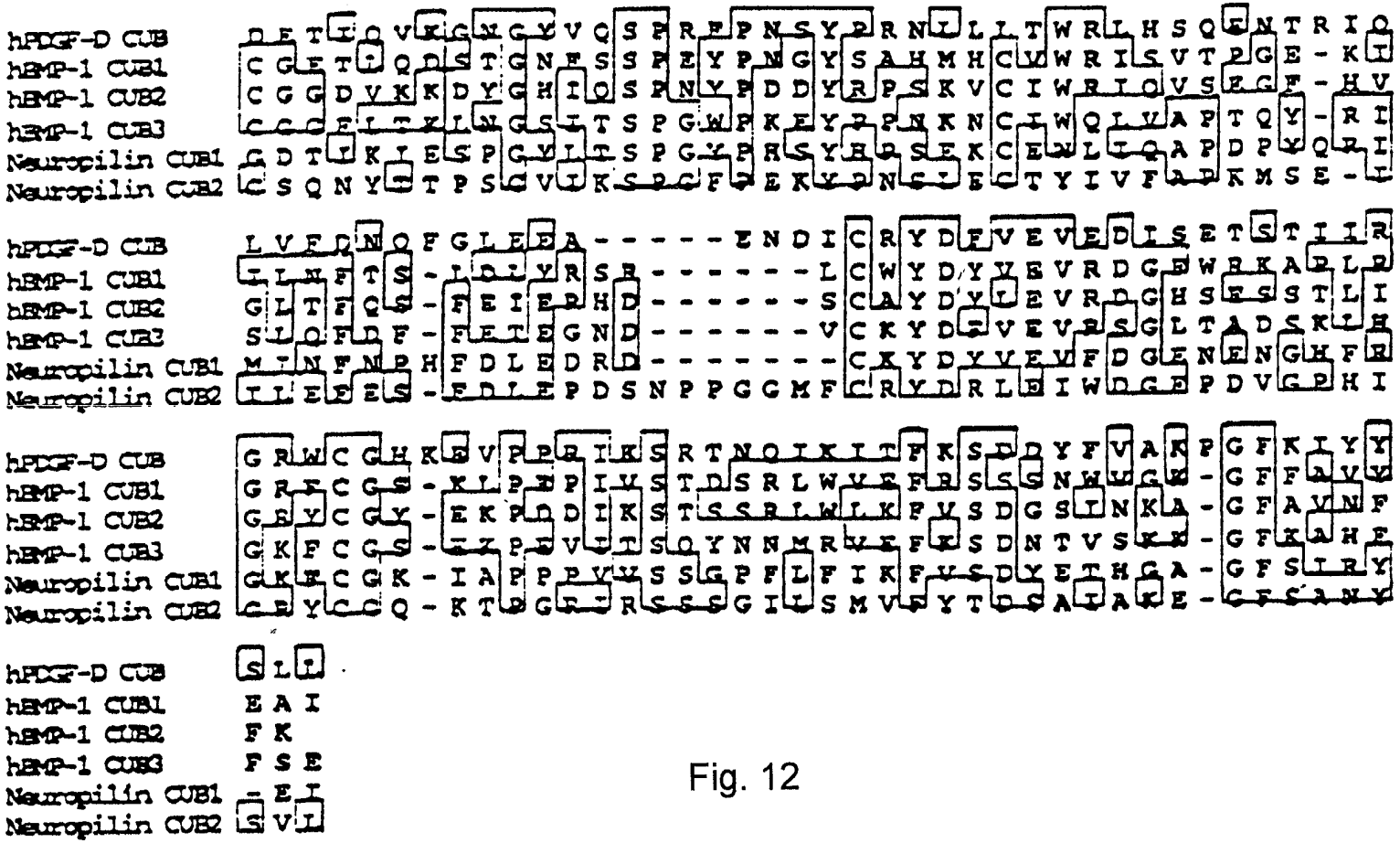

hPDGF-D CUB
hBMP-1 CUB1
hBMP-1 CUB2
hBMP-1 CUB3
Neuropilin CUB1
Neuropilin CUB2

Fig. 12

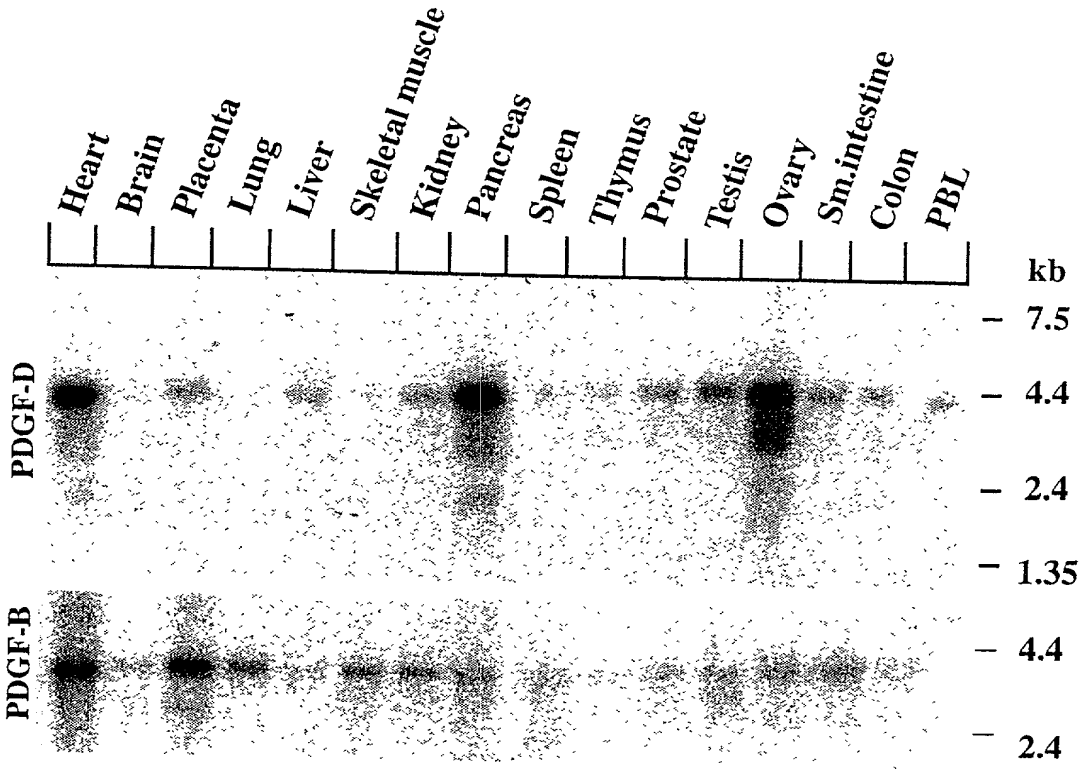

Heart
Brain
Placenta
Lung
Liver
Skeletal muscle
Kidney
Pancreas
Spleen
Thymus
Prostate
Testis
Ovary
Sm.intestine
Colon
PBL
kb
7.5
4.4
2.4
1.35
PDGF-D
PDGF-B
4.4
2.4

Fig. 14

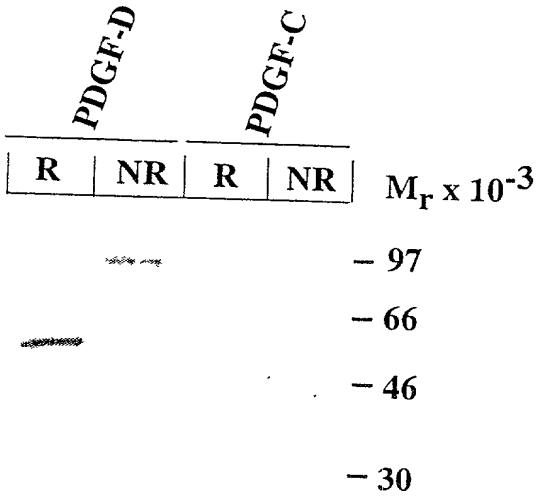

PDGF-D
PDGF-C
R
NR
R
NR
$M_r \times 10^{-3}$
97
66
46
30

Fig. 15

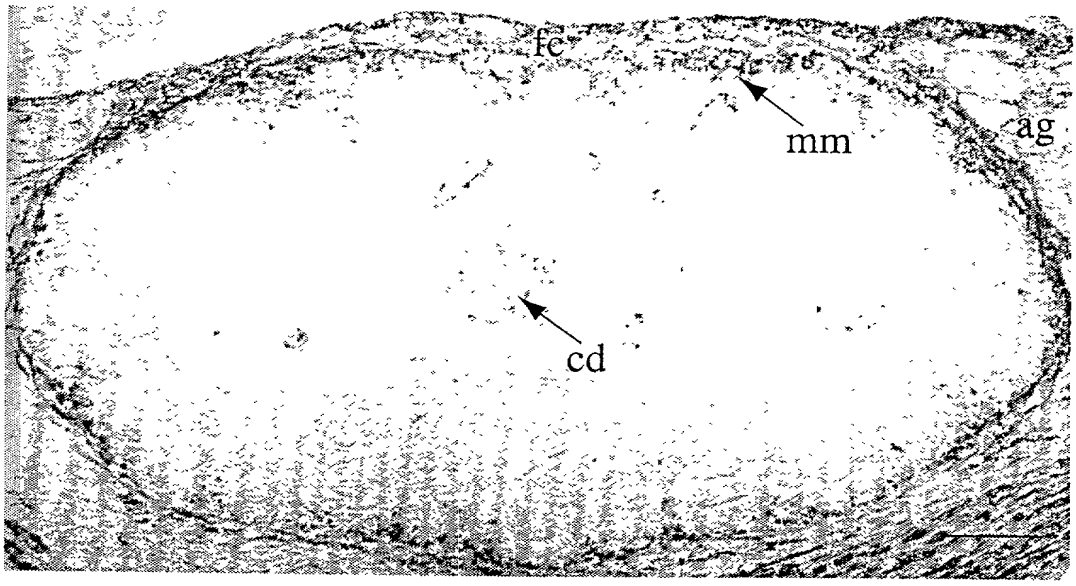


Fig. 16

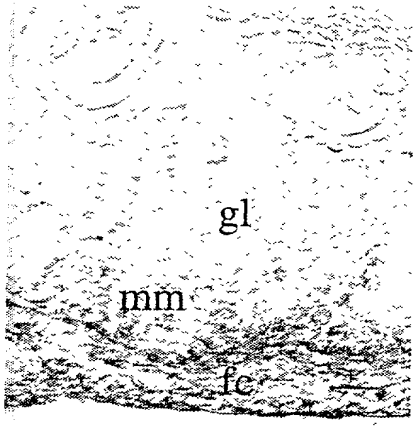


Fig. 17

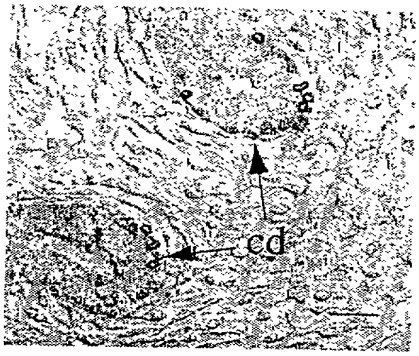


Fig. 18

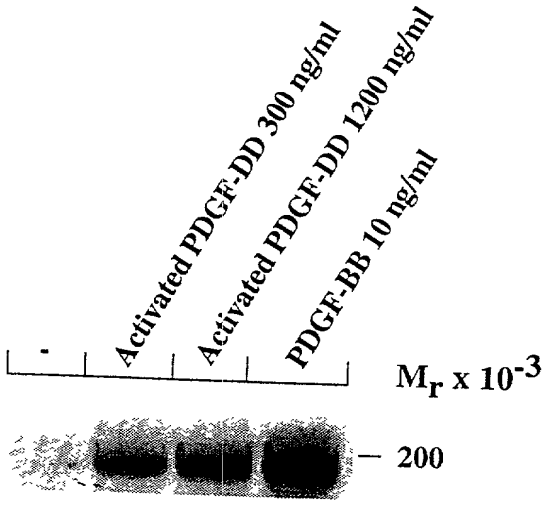

-
Activated PDGF-DD 300 ng/ml
Activated PDGF-DD 1200 ng/ml
PDGF-BB 10 ng/ml
M_r x 10^{-3}
200

Fig. 19

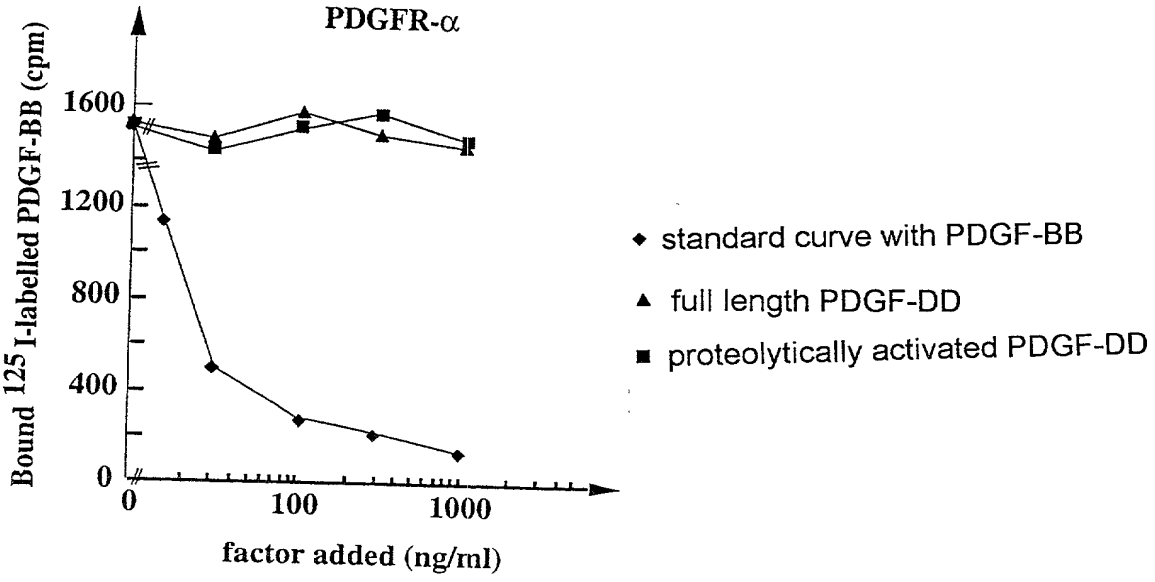

PDGFR-α
Bound ^{125}I-labelled PDGF-BB (cpm)
1600
1200
800
400
0
0
100
1000
factor added (ng/ml)
standard curve with PDGF-BB
full length PDGF-DD
proteolytically activated PDGF-DD

Fig. 20

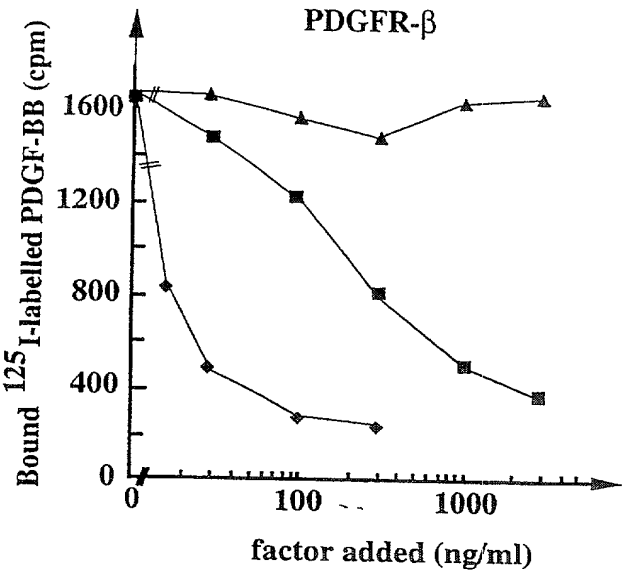


Fig. 21

Fig. 22A

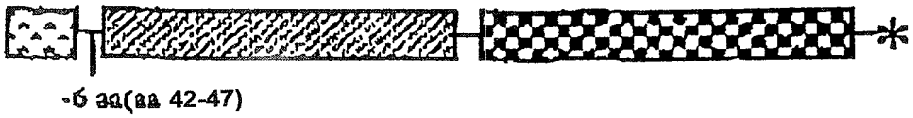


Fig. 22B

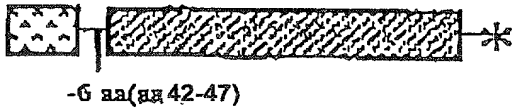
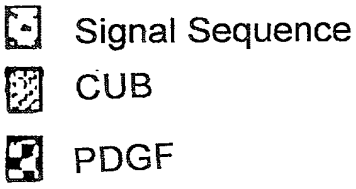


Fig. 22C



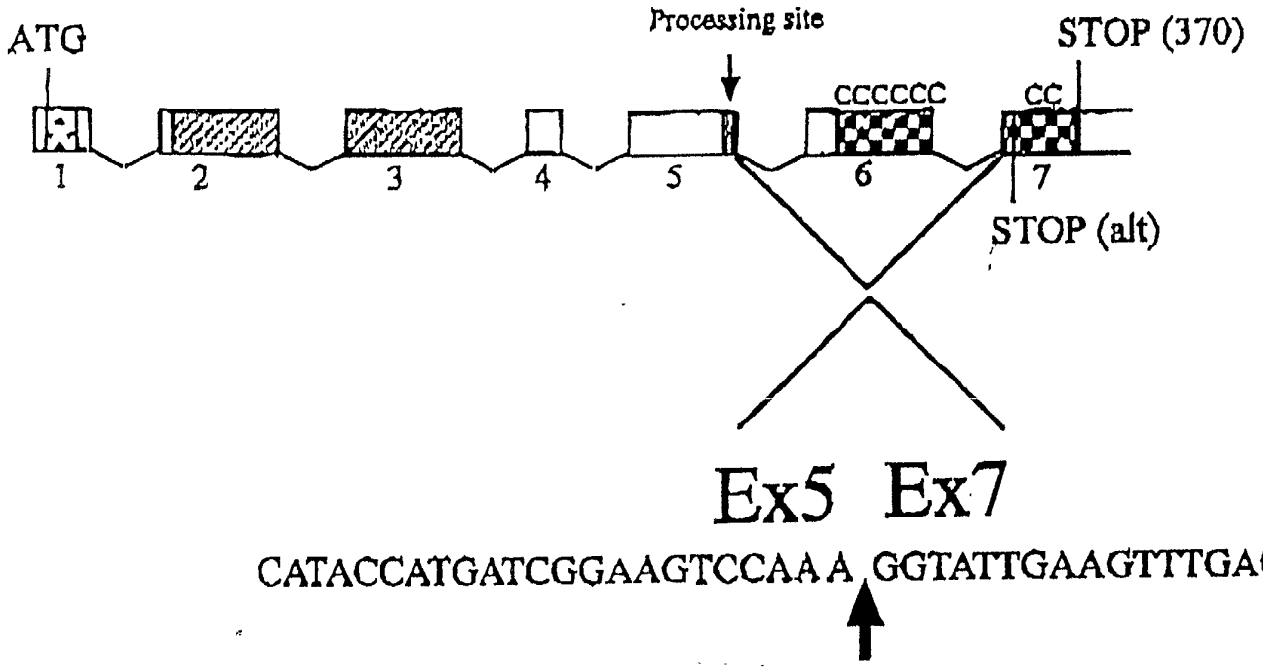


Fig. 23

Signal Sequence
CUB
PDGF

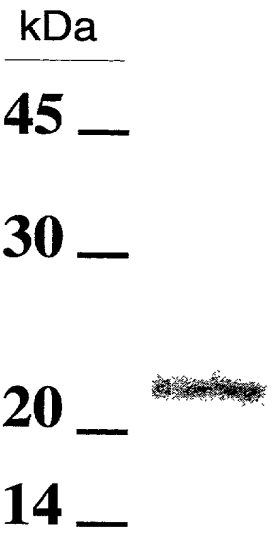
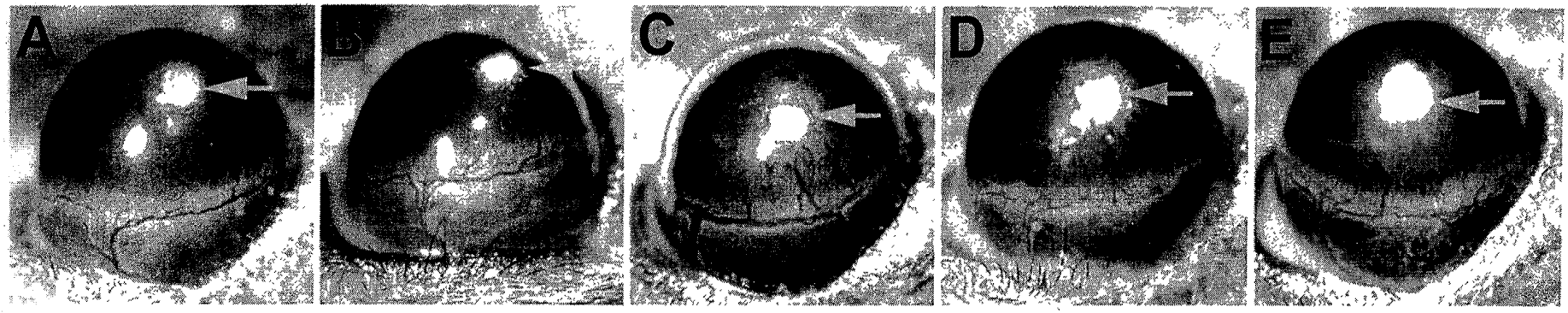


Fig. 24


A
B
C
D
E

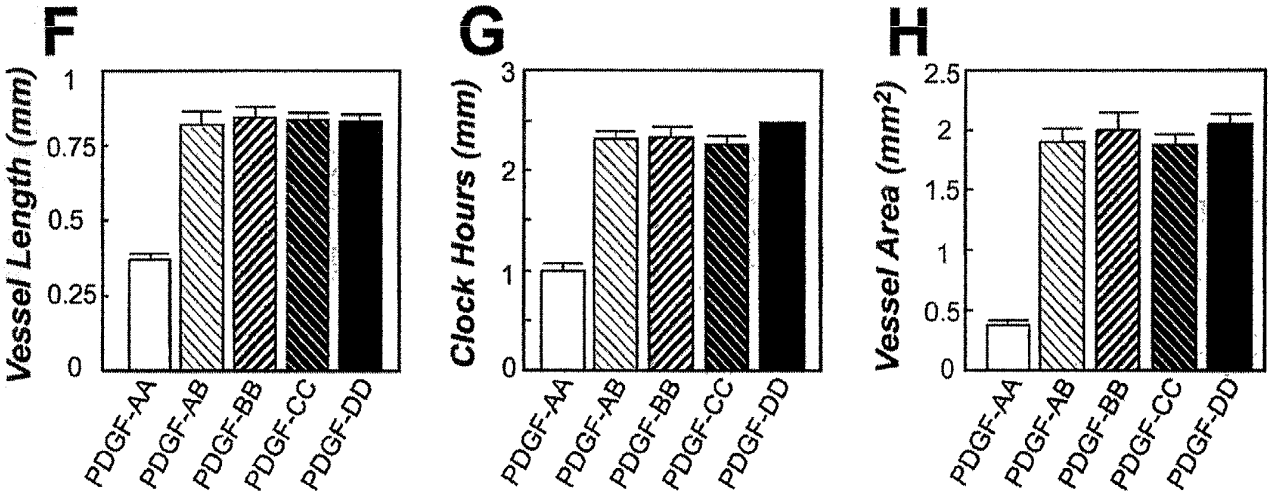

F
Vessel Length (mm)
1
0.75
0.5
0.25
0
PDGF-AA
PDGF-AB
PDGF-BB
PDGF-CC
PDGF-DD
G
Clock Hours (mm)
3
2
1
0
PDGF-AA
PDGF-AB
PDGF-BB
PDGF-CC
PDGF-DD
H
Vessel Area (mm2)
2.5
2
1.5
1
0.5
0
PDGF-AA
PDGF-AB
PDGF-BB
PDGF-CC
PDGF-DD

Fig. 25